of the foundations of functional analysis by reading this well-written book.

Selection of the material is of course the author's prerogative. In spite of my bias exhibited above, I highly recommend this attractive text for teaching and reference—particularly pedagogical reference. There is much to be learned from the author's considerable pedagogical skills.

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Chemical Biophysics: Quantitative Analysis of Cellular Systems. *By Daniel A. Beard and Hong Qian.* Cambridge University Press, New York, 2008. $80.00. xviii+311 pp., hardcover. ISBN 978-0-521-87070-2.

Numerous mathematical methods for quantitatively modeling and analyzing biophysical processes that underlie biological phenomena have been developed, and continue to be developed, in the field of computational biology. Such methods are essential in the pursuit of understanding how the components of cells, organs, and organisms interact and function as a dynamic system. Daniel Beard and Hong Qian have written an outstanding, comprehensive book about the methods used in computational biology. They are established leaders in the field [1, 2, 3], and their expertise is evident throughout the book.

The book consists of three main parts. The first part provides a foundation in physical chemistry for the treatment of biochemical reaction kinetics and thermodynamics. Concepts necessary to develop physically realistic models are emphasized beginning in Chapter 1 with fundamental principles from statistical thermodynamics. As the authors point out, statistical thermodynamics is a natural framework within which the current computational biology applications can be integrated into a consistent theory of biological systems. This approach provides a rigorous understanding of how the functions of a complex biological system can emerge from the integrated properties of its individual parts.

The authors have carefully crafted clear lines of reasoning in Chapter 1 to present only the essential concepts, while avoiding cluttering detail by dedicating the appendix (Chapter 12) to mathematical derivations from the statistical basis of thermodynamics. Chapter 2 provides an explanation of conventional notations and common calculations for biochemical systems. Chapter 3 discusses basic differential equation–based modeling of chemical kinetics in well-mixed systems and transport processes in cells and tissues. In this first part of the book, a clear connection is developed between the physical concepts and the mathematical methods discussed in the remainder of the text.

The second part of the book is the main body of the text, and it is where the authors focus on the primary methods used in computational biology to analyze and model biochemical systems. Chapter 4 is devoted to the all-important enzyme-catalyzed reactions. Topics in this chapter include a detailed account of Michaelis–Menten kinetics, directions for handling multiple enzyme binding sites, and an informative explanation of the King–Altman method for calculating nonequilibrium steady-state expressions for concentrations and fluxes in complex catalytic mechanisms. Chapters 5 and 6 apply the tools developed in Chapter 4 to small-scale systems (signal transduction networks) and large-scale

systems (biochemical reaction networks), respectively. Chapter 7 wraps up the second part of the book with an examination of kinetic models of membrane transport with special attention paid to coupled transport and reaction systems in metabolism and electrophysiology.

The third part of the book is a survey of special topics. Included in this collection are spatially distributed systems and reaction-diffusion models (Chapter 8), constraints-based optimization analysis of biochemical systems (Chapter 9), biomacromolecular structure and molecular association theory (Chapter 10), and stochastic modeling with the chemical master equation (Chapter 11). These areas of focus are all currently active areas of research in computational biology and are appropriately incorporated into the natural flow of the text. Every chapter draws on material from earlier chapters to systematically build the larger picture illustrating the usefulness and potential of the underlying methods.

This book is pedagogically clear, yet rigorous and challenging. Examples are presented throughout the text to emphasize important points and methodologies, to allow the exclusion of unnecessary proofs (as with the King–Altman method in Chapter 4), and to tie together methods from different chapters (as with the kinetic model of the TCA cycle in Chapter 6 and the oxidative phosphorylation model in Chapter 7). Exercises and references for additional reading are included at the end of each chapter to test understanding and encourage further interest. The book can be and has been used for an advanced undergraduate and graduate level semester-long course on computational biology. It could potentially be paired with another text, such as those by Athel Cornish-Bowden [4] or Christopher Fall et al. [5], to form a year-long sequence on biophysical chemistry.

I highly recommend this book to anyone interested in the field of computational biology as the most well-thought-out and broadly applicable text on the subject that I have read. You will profit from reading the authors' astute and accessible accounts of otherwise complex subjects and by keeping a copy of the book on your shelf for routine reference. This work is certainly deserving

of the praises it has received from esteemed individuals (and printed in the front matter of the book) as one of the most readable, useful, and indispensable accounts of biochemical thermodynamics and kinetics.

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From Hyperbolic Systems to Kinetic Theory: A Personalized Quest. *By Luc Tartar.* Springer-Verlag, Berlin, 2008. $74.95. xxviii+ 282 pp., softcover. ISBN 978-3-540-77561-4.

This text is unusual as math books go. Published by Springer as Lecture Notes of the Unione Matematica Italiana, it contains a series of 34 lectures taught by the author in the fall of 2001. Almost seven years passed before these lectures appeared in print.

The title is certainly correct. In fact, Tartar offers three books in one: first, an interesting and self-contained presentation of a significant fraction of the theories of hyperbolic conservation laws and the Boltzmann equation, with an emphasis on discrete velocity models; second, a footnote encyclopedia of "who's who" in the history of physics and mathematics, starting all the way back with Euclid and reaching to the present; and third, the "personalized